

1/6

1 TACTAAAGGG AACAAAAGCT GGAGCTCCAC CGCGGTGGCG GCCGCTCTAG AACTAGTGGA
ATGATTTCCTT TGTGTTTCGA CCTCGAGGTG GCGCCACCGC CGGCGAGATC TTGATCACCT
5' UTR

TCCCCCGGGC TGCAGGAATT CGGCACGAGG AACTTTCTGC CTCGTTTTTT TGCTCCTACT
AGGGGGCCCCG ACGTCCTTAA GCCGTGCTCC TTGAAAGACG GAGCAAAAAA ACGAGGATGA
5' UTR SEQ ID NO: 3

M S Q E I V Q S G Q T Y
GTTTTCTCT TCCAGTTTCT ACCATGTCGC AAGAAATTGT TCAATCAGGA CAAACCTACA
CAAAAAGAGA AGGTCAAAGA TGGTACAGCG TTCTTTAACA AGTTAGTCTT GTTTGGATGT
SEQ ID NO: 3

I I T N A K S G T V V D L S G E D N K S
TCATCACTAA CGCCAAATCC GGCACAGTTG TTGACCTTTC GGGCGAAGAC AACAAATCTA
AGTAGTGATT GCGGTTTAGG CCGTGTCAAC AACTGGAAAG CCCGCTTCTG TTGTTTAGAT
I I G F P K H G G T N Q R W T L N W T G
TTATTGGATT TCCCAAGCAT GGAGGAACAA ATCAGAGGTG GACCCTCAAC TGGACAGGGA
AATAACCTAA AGGGTTCGTA CCTCCTTGTT TAGTCTCCAC CTGGGAGTTG ACCTGTCCCT
SEQ ID NO: 5

K S W T F R S V S S E M Y L G L N G S P
AGAGTTGGAC TTTCCGCTCC GTTCTTCTG AAATGTATCT TGGCCTGAAT GGCTCGCCGT
TCTCAACCTG AAAGGCGAGG CAAAGAAGAC TTTACATAGA ACCGGACTTA CCGAGCGGCA
SEQ ID NO: 4 (partial)

SEQ ID NO: 5

SEQ ID NO: 6 (partial)

S D G T K L V A V T T P V E W R I W H
CTGATGGAAC AAACTGGTA GCCGTGACCA CCCCTGTTGA GTGGCGCATC TGGCACGA 418
GACTACCTTG TTTTGACCAT CGGCACTGGT GGGGACAACT CACCGCGTAG ACCGTGCT

FIG. 1

2/6

5' UTR

START
~~~  
M S Q E I  
1 GCCTCGTTTT TTGCTCCTA CTGTTTTTCT CTTCCAGTTT CTACCATGTC GCAAGAAATT  
CGGAGCAAAA AAACGAGGAT GACAAAAAGA GAAGGTCAAA GATGGTACAG CGTTCCTTAA  
  
V Q S G Q T Y I I T N A K S G T V V D L  
61 GTTCAATCAG GACAAACCTA CATCATCACT AACGCCAAAT CCGGCACAGT TGTTGACCTT  
CAAGTTAGTC CTGTTTGGAT GTAGTAGTGA TTGCGGTTTA GGCCGTGTCA ACAACTGGAA  
  
S G E D N K S I I G F P K H G G T N Q R  
121 TCGGGCGAAG ACAACAAATC TATTATTGGA TTCCCAAGC ATGGAGGAAC AAATCAGAGG  
AGCCCGCTTC TGTGTGTTAG ATAATAACCT AAAGGGTTCG TACCTCCTTG TTAGTCTCC  
  
W T L N W T G K S W  
181 TGGACCCTCA ACTGGACAGG GAAGAGTTGG A 211  
ACCTGGGAGT TGACCTGTCC CTTCTCAACC T

FIG. 2

3/6

```

      V D L   S G E   D N K   S I I G   F P K   H G G
1  TTGTTGACCT TTCGGGCGAA GACAACAAAT CTATTATTGG ATTTCCAAG CATGGAGGAA
   AACAACTGGA AAGCCCGCTT CTGTTGTTTA GATAATAACC TAAAGGGTTC GTACCTCCTT

      T N Q R   W T L   N W T   G K S W   T F R   S V S
61 CAAATCAGAG GTGGACCCTC AACTGGACAG GGAAGAGTTG GACTTCCGC TCCGTTTCTT
   GTTAGTCTC CACCTGGGAG TTGACCTGTC CCTTCTCAAC CTGAAAGGCG AGGCAAAGAA

      S E M Y   L G L   N G S   P S D G   T K L   V A V
121 CTGAAATGTA TCTTGGCCTG AATGGCTCGC CGTCTGATGG AACAAAAGTG GTAGCCGTGA
   GACTTTACAT AGAACCGGAC TTACCGAGCG GCAGACTACC TTGTTTTGAC CATCGGCACT

      T T P V   E W H   I W H   D E V D   P S T   Y R I
181 CCACCCCTGT TGAGTGGCAC ATCTGGCACG ACGAAGTTGA CCCTTCAACT TATCGTATCT
   GGTGGGGACA ACTCACCGTG TAGACCGTGC TGCTTCAACT GGAAGTTGA ATAGCATAGA

                                           A/G polymorphism
                                           ~
      F V P F   T T F   N M D   L Y A Q   G S A   A P G
241 TTGTACCTTT CACCACATTC AACATGGACC TCTACGCCCA RGGTAGTGCC GCCCCTGGTA
   AACATGGAAA GTGGTGTAAG TTGTACCTGG AGATGCGGGT YCCATCACGG CGGGGACCAT

                                           T/C polymorphism
                                           ~
      T P I T   T W Y   T W K   G I H Q   T W R   F E L
301 CGCTATCAC AACTTGGTAT ACATGGAAGG GYATCCACCA AACGTGGAGG TTTGAACTAG
   GCGGATAGTG TTGAACATA TGTACCTTCC CRTAGGTGGT TTGCACCTCC AAAGTTGATC

      T/G polymorphism
      ~
      STOP
      ~~~

 3' UTR
      ~~~~~~
A *
361 CTTAGGKTCA GGTTTCGGAT GTAATTTGTG TGTGTAAATC TTCTTGGACC ATGTTGTGCT
   GAATCCMAGT CCAAAGCCTA CATTAAACAC ACACATTTAG AAGAACCTGG TACAACACGA
                                           3' UTR
      ~~~~~~
421 TTTATTGTAC TCCGCTTGTT ATCATTATAC CCACCTATGT TGCAACATCT TTTTGGATCC
 AAATAACATG AGGCGAACAA TAGTAATATG GGTGGATACA ACGTTGTAGA AAAACCTAGG
 PolyA tail
      ~~~~~~
      3' UTR
      ~
481 CAAAAAAAAA AAA    493
   GTTTTTTTTT TTT

```

FIG. 3

4/6

START  
 ~~~  
 M S Q E I V Q S G Q T Y I I
 1 TCTCTTCCAG TTTCTACCAT GTCGCAAGAA ATTGTTCAAT CAGGACAAAC CTACATCATC
 AGAGAAGGTC AAAGATGGTA CAGCGTTCTT TAACAAGTTA GTCCTGTTTG GATGTAGTAG

T N A K S G T V V D L S G E D N K S I I
 61 ACTAACGCCA AATCCGGCAC AGTTGTTGAC CTTTCGGGCG AAGACAACAA ATCTATTATT
 TGATTGCGGT TTAGGCCGTG TCAACAACCTG GAAAGCCCGC TTCTGTTGTT TAGATAATAA

G F P K H G G T N Q R W T L N W T G K S
 121 GGATTTCCTA AGCATGGAGG AACAAATCAG AGGTGGACCC TCAACTGGAC AGGGAAGAGT
 CCTAAAGGGT TCGTACCTCC TTGTTTAGTC TCCACCTGGG AGTTGACCTG TCCCTTCTCA

W T F R S V S S E M Y L G L N G S P S D
 181 TGGACTTTCC GCTCCGTTTC TTCTGAAATG TATCTTGCC TGAATGGCTC GCCGTCTGAT
 ACCTGAAAGG CGAGGCAAAG AAGACTTTAC ATAGAACCGG ACTTACCGAG CGGCAGACTA

G T K L V A V T T P V E W H I W H D E V
 241 GGAACAAAAC TGGTAGCCGT GACCACCCCT GTTGAGTGGC ACATCTGGCA CGACGAAGTT
 CCTTGTTTTG ACCATCGGCA CTGGTGGGGA CAACTACCGG TGTAGACCGT GCTGCTTCAA

D P S T Y R I F V P F T T F N M D L Y A
 301 GACCCITCAA CTTATCGTAT CTTTGTACCT TTCACCACAT TCAACATGGA CCTCTACGCC
 CTGGGAAGTT GAATAGCATA GAAACATGGA AAGTGGTGTA AGTTGTACCT GGAGATGCGG

A/G polymorphism C/T polymorphism
 ~ ~
 Q G S A A P G T P I T T W Y T W K G I H
 361 CAAGGTAGTG CCGCCCCCTGG TACGCCTATC ACAACTTGGT ATACATGGAA GGGCATCCAC
 GTTCCATCAC GCGGGGGACC ATGCGGATAG TGTTGAACCA TATGTACCTT CCCGTAGGTG

G/T polymorphism
 ~
 STOP
 ~~~  
 Q T W R F E L A \*  
 421 CAAACGTGGA GGTTTGAAC AGCTTAGGGT CAGGTTTCGG ATGTAATTG T 491  
 GTTTCACCT CCAAACCTGA TCGAATCCCA GTCCAAAGCC TACATTAAAC A

FIG. 4

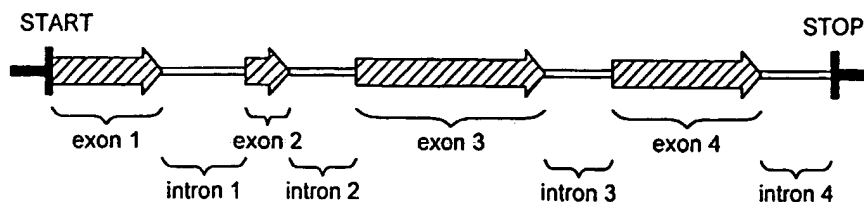


FIG. 5

5/6

## FIG. 6

START  
~ ~ ~

exon 1  
~~~~~  
M S Q E I V Q S G Q T Y I I
1 TCTCTTCCAG TTTCTACCAT GTCGCAAGAA ATTGTTCAAT CAGGACAAAC CTACATCATC
AGAGAAGGTC AAAGATGGTA CAGCGTTCTT TAACAAGTTA GTCCTGTTTG GATGTAGTAG

exon 1
~~~~~

intron 1  
~~~~~  
T N A K S G T V V D L S G E D N K S
61 ACTAACGCCA AATCCGGCAC AGTTGTTGAC CTTTCGGGCG AAGACAACAA ATCTAGTAAG
TGATTGCGGT TTAGGCCGTG TCAACAACAGT GAAAGCCCGC TTCTGTTGTT TAGATCATTC

intron 1
~~~~~

121 TCGTTTTTAG TCCCATGTTT TTTTGTGCA AAAAAAATTG ACTGACATAT TTTGTCTCCA  
AGCAAAAATC AGGGTACAAA AAAAAACAGT TTTTTTTAAC TGACTGTATA AAACAGAGGT

exon 2  
~~~~~

intron 1
~

intron 2
~~~~~

I G F P K H G G T N Q R  
181 GTTATTGGAT TTCCAAGCA TGGAGGAACA AATCAGAGGG TAGGTCTAGA AATGCACCTC  
CAATAACCTA AAGGGTTCGT ACCTCCTTGT TTAGTCTCCC ATCCAGATCT TTACGTGGAG

exon 3  
~~~~~

intron 2
~~~~~

W T L N W T G K S  
241 GTTAATATTG GTTTTTATTG ACATTTCATGA ACAGTGGACC CTCAACTGGA CAGGGAAGAG  
CAATTATAAC CAAAAATAAC TGTAAGTACT TGTCACCTGG GAGTTGACCT GTCCTTCTC

exon 3  
~~~~~

W T F R S V S S E M Y L G L N G S P S D
301 TTGGACTTTC CGCTCCGTTT CTTCTGAAAT GTATCTTGGC CTGAATGGCT CGCCGTCTGA
AACCTGAAAG GCGAGGCAAA GAAGACTTCA CATAGAACCG GACTTACCGA GCGGCAGACT

exon 3
~~~~~

G T K L V A V T T P V E W H I W H D E V  
361 TGGAACAAAA CTGGTAGCCG TGACCACCCC TGTGAGTGG CACATCTGGC ACGACGAAAGT  
ACCTTGTTTT GACCATCGGC ACTGGTGGGG ACAACTCACC GTGTAGACCG TGCTGCTTCA

6/6

```

      exon 3                      intron 3
-----
      D P S T Y
421  TGACCCTTCA ACTTATCGGT GAGTCCCCTA AATATTACTT GCTTGTGGTT CATACTAATA
      ACTGGGAAGT TGAATAGCCA CTCAGGGGAT TTATAATGAA CGAACACCAA GTATGATTAT

      intron 3                      exon 4
-----
      I F V P F T T F N M D L Y A Q G
481  CGTCGTTCGA AGTATCTTTG TACCTTTCAC CACATTCAAC ATGGACCTCT ACGCCCAGGG
      GCAGCAAGCT TCATAGAAAC ATGGAAAGTG GTGTAAGTTG TACCTGGAGA TGCGGGTCCC

      exon 4
-----
      S A A P G T P I T T W Y T W K G I H Q T
541  TAGTGCCGCC CCTGGTACGC CTATCACAAC TTGGTATACA TGGAAGGGTA TCCACCAAAC
      ATCACGGCGG GGACCATGCG GATAGTGTTG AACCATATGT ACCTTCCCAT AGGTGGTTTG

      intron 4
-----

      exon 4
-----
      W R F E L
601  GTGGAGGTTT GAACTAGGTA GGGCTTGCGA TCTACCCCGG ATCCTCCATG AACTAATGTG
      CACCTCCAAA CTGATCCAT CCCGAACGCT AGAGTGGGCC TAGGAGGTAC TTGATTACAC

      intron 4                      STOP
-----
661  ATCACGTCGT GTTCTAGCTT AGGTTGAGGT TTCGGATGTA ATTTGT      706
      TAGTGCAGCA CAAGATCGAA TCCAAGTCCA AAGCCTACAT TAAACA

```

FIG. 6 CONT'D